

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/524,652  
Source: PCT  
Date Processed by STIC: 2-26-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/524/652

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS WHICH WERE INSERTED BY PTO SOFTWARE

1 \_\_\_\_\_ Wrapped Nucleics  
\_\_\_\_\_ Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .5; this will prevent "wrapping."

2 \_\_\_\_\_ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 \_\_\_\_\_ Misaligned Amino  
\_\_\_\_\_ Numbering

The numbering under each 5' amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 \_\_\_\_\_ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 \_\_\_\_\_ Variable Length

Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 \_\_\_\_\_ PatentIn 2.0  
\_\_\_\_\_ "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 \_\_\_\_\_ Skipped Sequences  
(OLD RULES)

Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)  
(ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequence.

8 \_\_\_\_\_ Skipped Sequences  
(NEW RULES)

Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000

9 \_\_\_\_\_ Use of n's or Xaa's  
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 \_\_\_\_\_ Invalid <21>  
\_\_\_\_\_ Response

Per 1.823 of Sequence Rules, the only valid <21> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <21> response is Unknown.

11 \_\_\_\_\_ Use of <220>

Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
Use of <220> to <223> is MANDATORY if <21> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 \_\_\_\_\_ PatentIn 2.0  
\_\_\_\_\_ "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 \_\_\_\_\_ Misuse of n/Xaa

"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

## RAW SEQUENCE LISTING

DATE: 02/26/2005

PATENT APPLICATION: US/10/524,652

TIME: 10:54:35

Input Set : A:\Sequence Listing - Docket No 13173-00001 US.txt

Output Set: N:\CRF4\02262005\J524652.raw

3 <110> APPLICANT: Schopfer, Christel R  
 4 Flachmann, Ralf  
 5 Herbers, Karin  
 6 Kunze, Irene  
 7 Sauer, Matt  
 8 Klebsattel, Martin  
 10 <120> TITLE OF INVENTION: A process for preparing zeaxanthin and/or biosynthetic  
 11 intermediates and/or secondary products thereof  
 13 <130> FILE REFERENCE: 13173-00001-US  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/524,652  
 C--> 15 <141> CURRENT FILING DATE: 2005-02-17  
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP 03/009105  
 16 <151> PRIOR FILING DATE: 2003-08-18  
 18 <150> PRIOR APPLICATION NUMBER: DE 102 38 980.2  
 19 <151> PRIOR FILING DATE: 2002-08-20  
 21 <150> PRIOR APPLICATION NUMBER: DE 102 38 978.0  
 22 <151> PRIOR FILING DATE: 2002-08-20  
 24 <150> PRIOR APPLICATION NUMBER: DE 102 38 979.9  
 25 <151> PRIOR FILING DATE: 2002-08-20  
 27 <150> PRIOR APPLICATION NUMBER: DE 102 53 112.9  
 28 <151> PRIOR FILING DATE: 2002-11-13  
 30 <150> PRIOR APPLICATION NUMBER: DE 102 58 971.2  
 31 <151> PRIOR FILING DATE: 2002-12-16  
 33 <160> NUMBER OF SEQ ID NOS: 43  
 35 <170> SOFTWARE: PatentIn version 3.3  
 37 <210> SEQ ID NO: 1  
 38 <211> LENGTH: 777  
 39 <212> TYPE: DNA  
 40 <213> ORGANISM: Arabidopsis thaliana  
 42 <220> FEATURE:  
 43 <221> NAME/KEY: promoter  
 44 <222> LOCATION: (1)..(777)  
 47 <400> SEQUENCE: 1  
 48 gagctcactc actgatttcc attgcttgaa aattgatgat gaactaagat caatccatgt 60  
 50 tagtttcaaa acaacagtaa ctgtggccaa cttagttttg aaacaacact aactggtcga 120  
 52 agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactgttt ggagtttagga 180  
 54 ccaaacatta tctacaaaca aagacttttc tcctaacttg tgattccttc ttaaacccta 240  
 56 ggggtaatat tctattttcc aaggatcttt agttaaaaggc aaatccggga aattattgta 300  
 58 atcatttggy gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360  
 60 tatatatctc ttcttcttca ttcccaaat taacagacaa aagtagaata ttggctttta 420  
 62 acaccaatat aaaaacttgc ttcacaccta aacacttttg tttactttag ggtaagtgc 480  
 64 aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt 540  
 66 ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta 600

Does Not Comply  
 Corrected Diskette Needed  
 (p3.2)

## RAW SEQUENCE LISTING

DATE: 02/26/2005

PATENT APPLICATION: US/10/524,652

TIME: 10:54:35

Input Set : A:\Sequence Listing - Docket No 13173-00001 US.txt

Output Set: N:\CRF4\02262005\J524652.raw

68 tcaacttagtt ttcatacaact tetgaactta cctttcatgg attaggcaat actttccatt 660  
 70 tttagtaact caagtggacc ctttacttct tcaactccat ctctctcttt ctatttcact 720  
 72 tctttcttct cattatatct cttgtcctct ccaccaaatc tcttcaacaa aaagctt 777  
 75 <210> SEQ ID NO: 2  
 76 <211> LENGTH: 195  
 77 <212> TYPE: DNA  
 78 <213> ORGANISM: Potato  
 80 <220> FEATURE:  
 81 <221> NAME/KEY: Intron  
 82 <222> LOCATION: (1)..(195)  
 85 <400> SEQUENCE: 2  
 86 tacgtaagtt tctgcttcta cctttgatat atatataata attatcatta attagtagta 60  
 88 atataatatt tcaaataattt ttttcaaaat aaaagaatgt agtatatagc aattgctttt 120  
 90 ctgtagttta taagtgtgta tattttaatt tataactttt ctaatatatg accaaaattt 180  
 92 gttgatgtgc agctg 195  
 95 <210> SEQ ID NO: 3  
 96 <211> LENGTH: 212  
 97 <212> TYPE: DNA  
 98 <213> ORGANISM: artificial sequence  
 100 <220> FEATURE:  
 101 <221> NAME/KEY: Intron  
 102 <222> LOCATION: (1)..(212)  
 103 <223> OTHER INFORMATION: Intron  
 106 <400> SEQUENCE: 3  
 107 gtcgactacg taagtttctg cttctacctt tgatatatat ataataatta tcattaatta 60  
 109 gtagtaatat aatatttcaa atattttttt caaaataaaa gaatgtagta tatagcaatt 120  
 111 gcttttctgt agtttataag tgtgtatatt ttaatttata acttttctaa tatatgacca 180  
 113 aaatttggtg atgtgcaggt atcaccggat cc 212  
 116 <210> SEQ ID NO: 4  
 117 <211> LENGTH: 1830  
 118 <212> TYPE: DNA  
 119 <213> ORGANISM: Tagetes erecta  
 121 <220> FEATURE:  
 122 <221> NAME/KEY: CDS  
 123 <222> LOCATION: (141)..(1691)  
 126 <400> SEQUENCE: 4  
 127 ggcacgaggc aaagcaaagg ttgtttgttg ttgttgttga gagacactcc aatccaaaca 60  
 129 gatacaaggc gtgactggat atttctctct cgttcctaac aacagcaacg aagaagaaaa 120  
 131 agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca 173  
 132 Met Ser Met Arg Ala Gly His Met Thr Ala Thr  
 133 1 5 10  
 135 atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg 221  
 136 Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr  
 137 15 20 25  
 139 aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa 269  
 140 Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln  
 141 30 35 40  
 143 gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tgc gag ctg 317  
 144 Glu Ile Glu Glu Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu

pls explain source  
 Invalid of genetic material.  
 response

see  
 item  
 #11 on  
 error  
 summary  
 sheet

The type of errors shown exist throughout  
 the sequence listing. Please check subsequent  
 sequences for similar errors.

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TIME: 10:54:35

Input Set : A:\Sequence Listing - Docket No 13173-00001 US.txt

Output Set: N:\CRF4\02262005\J524652.raw

145	45	50	55	
147	ctt ttt gtt caa atg caa cag aat aag tcc atg gat gca cag tct agc	365		
148	Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser			
149	60 65 70 75			
151	cta tcc caa aag ctc cca agg gta cca ata gga gga gga gga gac agt	413		
152	Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser			
153	80 85 90			
155	aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt	461		
156	Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu			
157	95 100 105			
159	gct ctt gct gga gaa tca gcc aag cta ggc ttg aat gtc gca ctt atc	509		
160	Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile			
161	110 115 120			
163	ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa	557		
164	Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu			
165	125 130 135			
167	ttt ata ggt ctt gga ctt gag ggc tgt att gaa cat gtt tgg cga gat	605		
168	Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp			
169	140 145 150 155			
171	act gta gta tat ctt gat gac aac gat ccc att ctc ata ggt cgt gcc	653		
172	Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala			
173	160 165 170			
175	tat gga cga gtt agt cgt gat tta ctt cac gag gag ttg ttg act agg	701		
176	Tyr Gly Arg Val Ser Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg			
177	175 180 185			
179	tgc atg gag tca ggc gtt tca tat ctg agc tcc aaa gtg gaa cgg att	749		
180	Cys Met Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile			
181	190 195 200			
183	act gaa gct cca aat ggc cta agt ctc ata gag tgt gaa ggc aat atc	797		
184	Thr Glu Ala Pro Asn Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile			
185	205 210 215			
187	aca att cca tgc agg ctt gct act gtc gct tct gga gca gct tct gga	845		
188	Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly			
189	220 225 230 235			
191	aaa ctt ttg cag tat gaa ctt ggc ggt ccc cgt gtt tgc gtt caa aca	893		
192	Lys Leu Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr			
193	240 245 250			
195	gct tat ggt ata gag gtt gag gtt gaa agc ata ccc tat gat cca agc	941		
196	Ala Tyr Gly Ile Glu Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser			
197	255 260 265			
199	cta atg gtt ttc atg gat tat aga gac tac acc aaa cat aaa tct caa	989		
200	Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln			
201	270 275 280			
203	tca cta gaa gca caa tat cca aca ttt ttg tat gtc atg cca atg tct	1037		
204	Ser Leu Glu Ala Gln Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser			
205	285 290 295			
207	cca act aaa gta ttc ttt gag gaa act tgt ttg gct tca aaa gag gcc	1085		
208	Pro Thr Lys Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala			
209	300 305 310 315			

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211 atg cct ttt gag tta ttg aag aca aaa ctc atg tca aga tta aag act      1133
212 Met Pro Phe Glu Leu Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr
213           320           325           330
215 atg ggg atc cga ata acc aaa act tat gaa gag gaa tgg tca tat att      1181
216 Met Gly Ile Arg Ile Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile
217           335           340           345
219 cca gta ggt gga tcc tta cca aat acc gag caa aag aac ctt gca ttt      1229
220 Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe
221           350           355           360
223 ggt gct gct gct agc atg gtg cat cca gcc aca gga tat tcg gtt gta      1277
224 Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val
225           365           370           375
227 aga tca ctg tca gaa gct cct aat tat gca gca gta att gca aag att      1325
228 Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile
229 380           385           390           395
231 tta ggg aaa gga aat tca aaa cag atg ctt gat cat gga aga tac aca      1373
232 Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr
233           400           405           410
235 acc aac atc tca aag caa gct tgg gaa aca ctt tgg ccc ctt gaa agg      1421
236 Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg
237           415           420           425
239 aaa aga cag aga gca ttc ttt ctc ttt gga tta gca ctg att gtc cag      1469
240 Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln
241           430           435           440
243 atg gat att gag ggg acc cgc aca ttc ttc cgg act ttc ttc cgc ttg      1517
244 Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu
245           445           450           455
247 ccc aca tgg atg tgg tgg ggg ttt ctt gga tct tcg tta tca tca act      1565
248 Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr
249 460           465           470           475
251 gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg cat agc      1613
252 Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser
253           480           485           490
255 ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca gga gga      1661
256 Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly
257           495           500           505
259 aca atg tta aaa gcg tat ctc acg ata taa ataactctag tcgcgatcag      1711
260 Thr Met Leu Lys Ala Tyr Leu Thr Ile
261           510           515
263 tttagattat aggcacatct tgcatatata tatgtataaa ccttatgtgt gctgtatcct      1771
265 tacatcaaca cagtcattaa ttgtatttct tggggtaatg ctgatgaagt attttctgg      1830
268 <210> SEQ ID NO: 5
269 <211> LENGTH: 516
270 <212> TYPE: PRT
271 <213> ORGANISM: Tagetes erecta
273 <400> SEQUENCE: 5
275 Met Ser Met Arg Ala Gly His Met Thr Ala Thr Met Ala Ala Phe Thr
276 1           5           10           15
279 Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys

```

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Input Set : A:\Sequence Listing - Docket No 13173-00001 US.txt

Output Set: N:\CRF4\02262005\J524652.raw

280	20	25	30
283 Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu			
284 35 40 45			
287 Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met			
288 50 55 60			
291 Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu			
292 65 70 75 80			
295 Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp			
296 85 90 95			
299 Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu			
300 100 105 110			
303 Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro			
304 115 120 125			
307 Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly			
308 130 135 140			
311 Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu			
312 145 150 155 160			
315 Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser			
316 165 170 175			
319 Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly			
320 180 185 190			
323 Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn			
324 195 200 205			
327 Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg			
328 210 215 220			
331 Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr			
332 225 230 235 240			
335 Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Ile Glu			
336 245 250 255			
339 Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met			
340 260 265 270			
343 Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln			
344 275 280 285			
347 Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe			
348 290 295 300			
351 Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu			
352 305 310 315 320			
355 Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile			
356 325 330 335			
359 Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser			
360 340 345 350			
363 Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser			
364 355 360 365			
367 Met Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu			
368 370 375 380			
371 Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile Leu Gly Lys Gly Asn			
372 385 390 395 400			
375 Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr Thr Asn Ile Ser Lys			
376 405 410 415			

VERIFICATION SUMMARY

DATE: 02/26/2005

PATENT APPLICATION: US/10/524,652

TIME: 10:54:36

Input Set : A:\Sequence Listing - Docket No 13173-00001 US.txt

Output Set: N:\CRF4\02262005\J524652.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date